

FIGURE 1

EXPRESS MAIL
EE360933802US
ATTY. DKT. 266/186
SHEET 2 OF 12

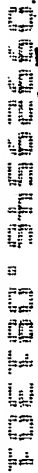


FIGURE 2

EXPRESS MAIL
EL360933802US
ATTY. DKT. 266/186
SHEET 3 OF 12



09929545-081304

FIGURE 3

EXPRESS MAIL
EL360933802US
ATTY. DKT. 266/186
SHEET 4 OF 12

Jc879 US PTO
09/929546
08/13/01

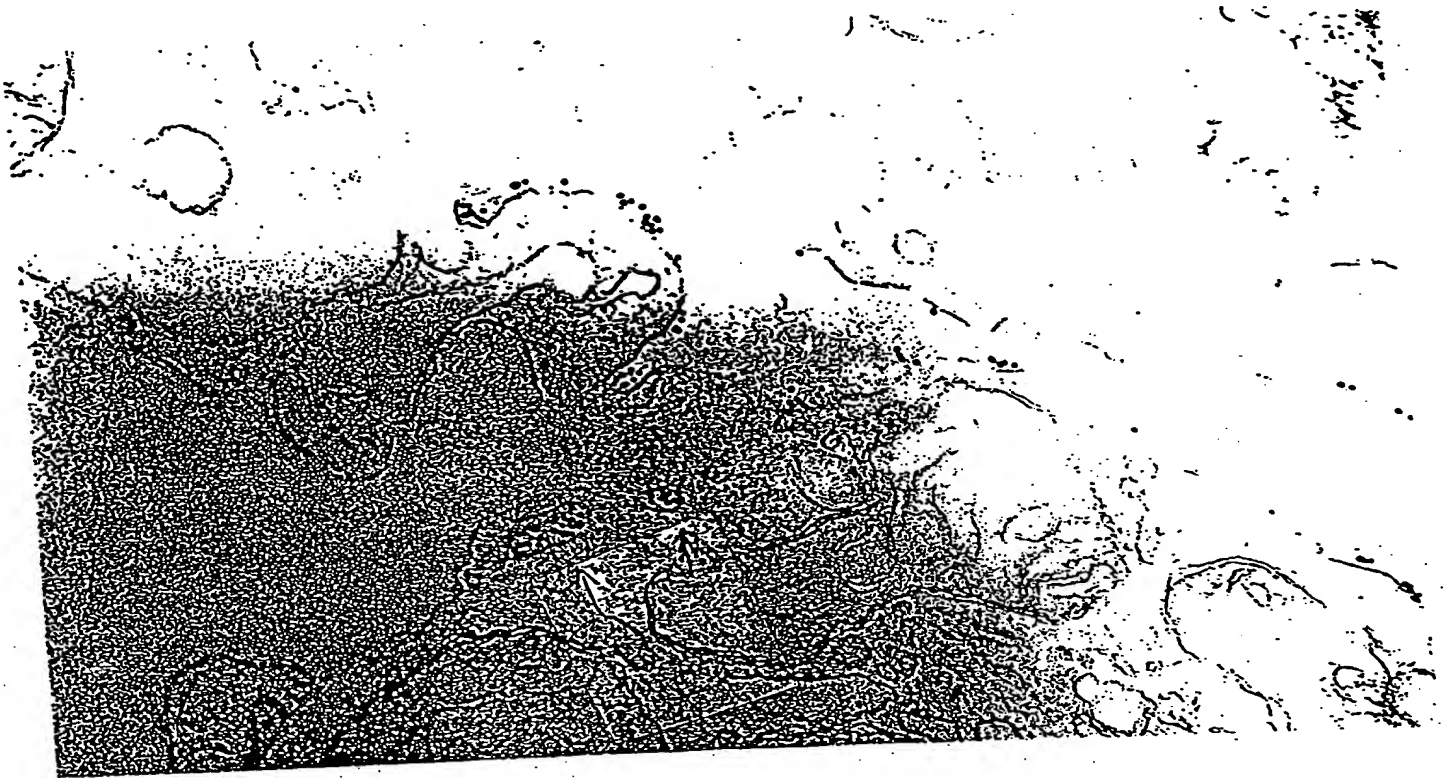


FIGURE 4



FIGURE 5

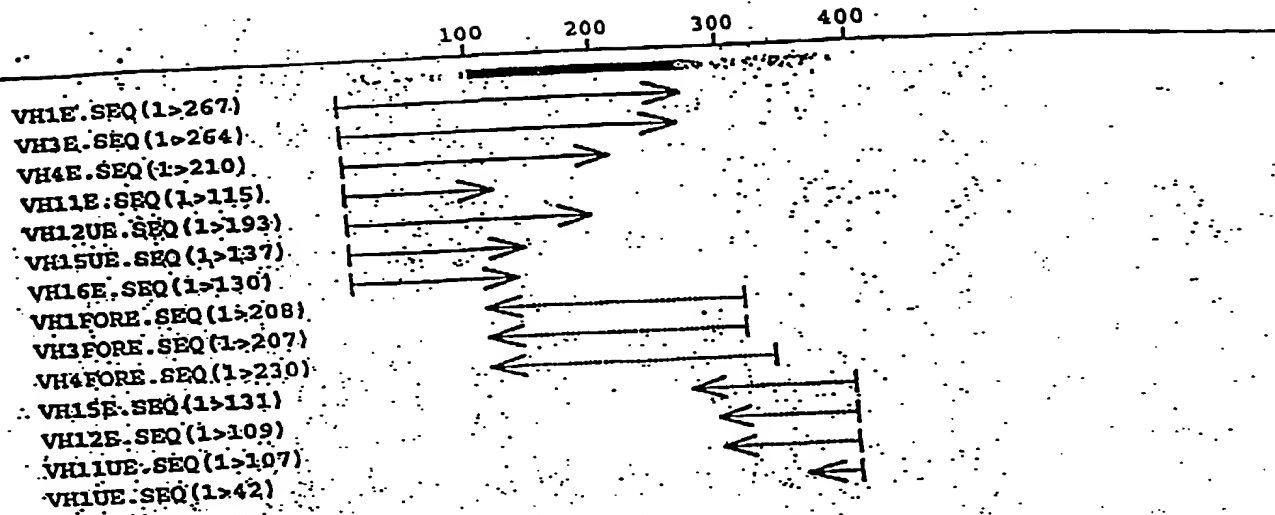


FIGURE 6

Enzymes : All 74 enzymes (No Filter)
Settings: Linear, Certain Sites Only, Standard Genetic Code

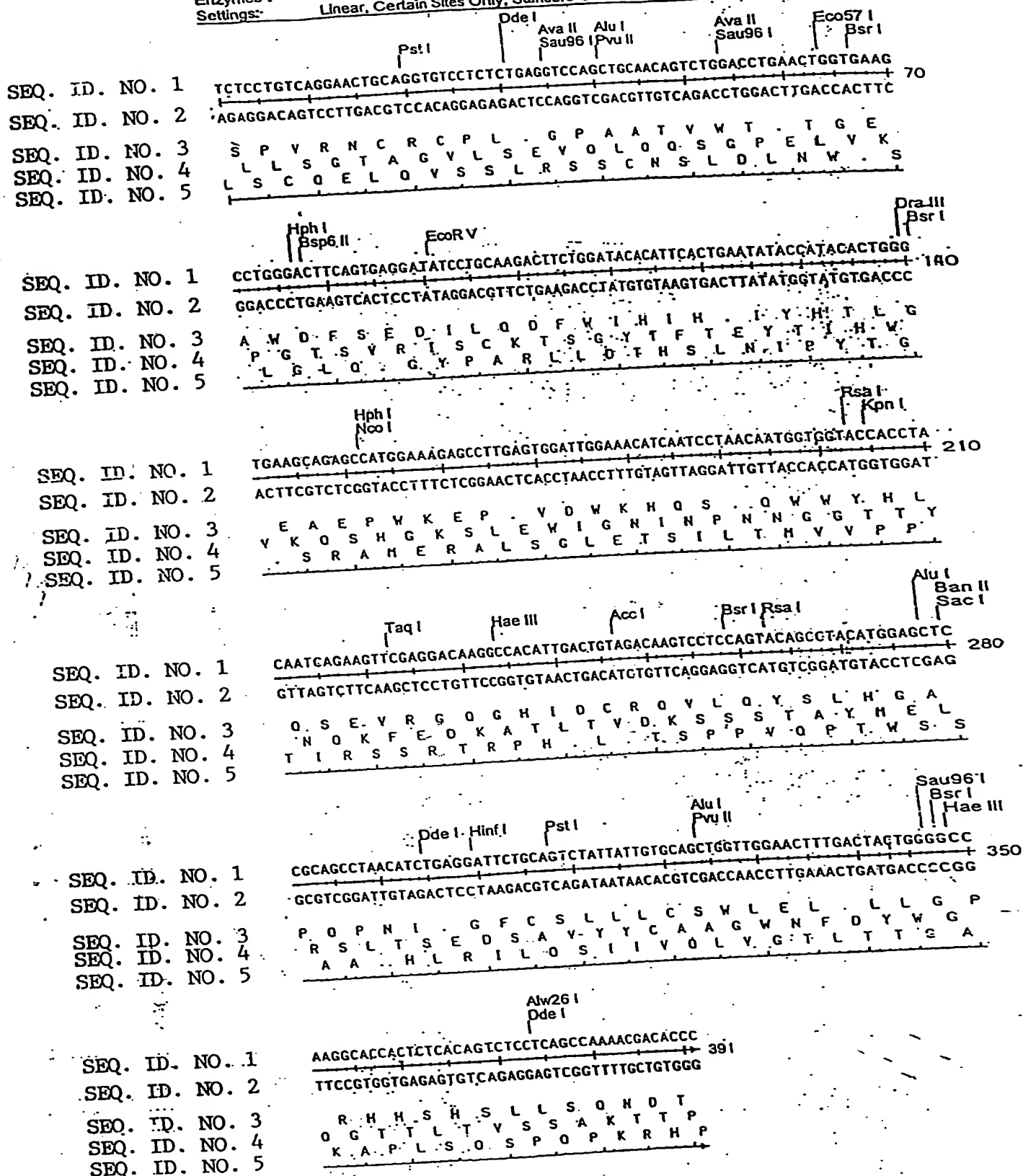


FIGURE 7

Lipman-Pearson Protein Alignment

Ktuple: 2; Gap Penalty: 4; Gap Length Penalty: 12.

Seq1(1>115)	Seq2(1>125)	Similarity Index	Gap Number	Gap Length	Consensus Length
J591VH.PRO	MUVHIA.PRO	75.6	2	10	125
(1>115)	(1>125)				

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      10      20      30      40      50
EVQLQQSGPELVKPGT SVRI SCKTSGYTFIEYTI-HWVKQSHGKSLEWIGNINPNNGGTT
EVQLQQSGPELVKPG:SV:ISCK:SGYTFT:Y :WVKQS.GKSLEWIG:INP.NGGT:
EVQLQQSGPELVKPGASVKISCKASGYTFTDYYMNNWVKOSPGKSLEWIGDINPGNGGTS
      10      20      30      40      50      60
YNQKFEDKATLTVDKSSSTAYMELRSLTSEDSAVYYCAAG-----WNFDYWGQGTT
YNQKF:KATLTVDKSSSTAYM:L.SLTSEDSAVYYCA:G.FDYWGQGTT
YNQKFKGKATLTVDKSSSTAYMQLSSLTSEDSAVYYCARGYYSSSYMAYYAFDYWGQGTT
      70      80      90      100      110      120
LTVSS
:TVSS
:TVSS

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FIGURE 8

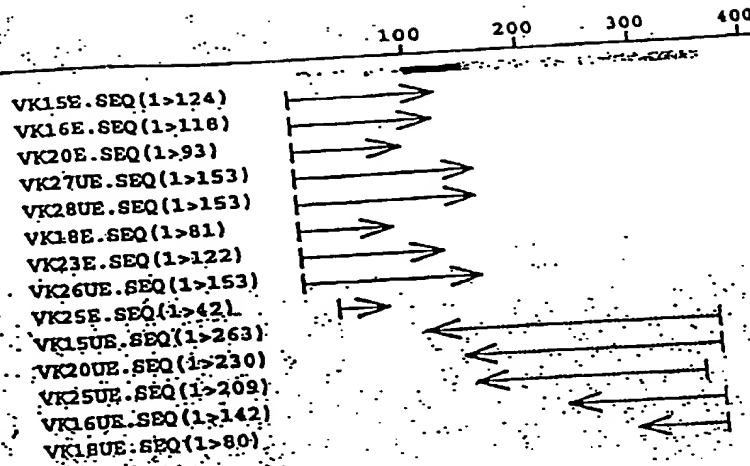


FIGURE 9

Enzymes: All 74 enzymes (No Filter)
 Settings: Linear, Certain Sites Only, Standard Genetic Code

SEQ. ID. NO. 9 TTATATGGAGCTGATGGGAACATTGTAATGACCAATCTCCAAATCCATGTCCATGTCAGTAGGAGAGA 70
 SEQ. ID. NO. 10 AATATACCTCGACTACCCCTTGTAACATTACTGGGTTAGAGGGTTAGGTACAGGTACAGTCATCCTCTCT
 SEQ. ID. NO. 11 L Y G A D G N I V H T Q S P K S H S H S V G E
 SEQ. ID. NO. 12 Y H E L H G T L P N L P N P C P C Q E R
 SEQ. ID. NO. 13 I I W S W E H C N D P I S O I H V H V S R R E

SEQ. ID. NO. 9 GGGTCACCTGACCTGCAAGGCCAGTGAGAATGTGGTACTTATGTTTCCTGGTATCAACAGAAACCAGA 140
 SEQ. ID. NO. 10 CCCAGTGGAAGTGGACGTTCCGGTCACTCTTACACCAATGAATACAAAGGACCATAGTTGTCTTGGTCT
 SEQ. ID. NO. 11 R V T L T C K A S E N V V T Y V S Y Y Q Q K P E
 SEQ. ID. NO. 12 G S P P A R P V R H V L L H F P G I N R N Q
 SEQ. ID. NO. 13 G H L D L Q G Q E C G Y L C F L Y S T E T R

SEQ. ID. NO. 9 GCAGTCTCTAACTGCTGATATACGGGGCATCCAACCGGTACACTGGGGTCCCCGATCGCTTCACAGGC 210
 SEQ. ID. NO. 10 CGTCAGAGGATTGACGACTATATGCCCGTAGGTTGGCCATGTGACCCAGGGGCTAGCGAAGTGTCCG
 SEQ. ID. NO. 11 Q S P K L L I Y G A S N R Y T G V P D R F T G
 SEQ. ID. NO. 12 S S L L N C Y T G H P T G T L G S P I A S Q A
 SEQ. ID. NO. 13 A V S T A D I R G I Q P V H W G P R S L H R

SEQ. ID. NO. 9 AGTGGATCTGCAACAGATTTCACCTGACCATCAGCAGTGTGCAGGCTGAAGACCTTGCAGATTATCACT 280
 SEQ. ID. NO. 10 TCACCTAGACGTTGTCTAAAGTGAGACTGGTAGTCGTACACGTCGCACTTCTGGAACGTCTAATAGTGA
 SEQ. ID. NO. 11 S G S A T O F T L T I S S V Q A E D L A D Y H
 SEQ. ID. NO. 12 V D L Q Q I S L P S A V C R L K T L Q I I T
 SEQ. ID. NO. 13 Q W I C N R F H S O H Q Q C A G R P C R L S L

SEQ. ID. NO. 9 GTGGACAGGGTTACAGCTATCCGTACACGTTCCGAGGGGGACCAAGCTGGAAATAAAACGGGCTGATGC 350
 SEQ. ID. NO. 10 CACCTGTCCCAATGTGATAGGCATGTGCAAGCCTCCCGCTGGTTCGACCTTTATTTGCCCGACTACG
 SEQ. ID. NO. 11 C G G G Y S Y P Y T F G G G T K L E I K R A D A
 SEQ. ID. NO. 12 V D R V T A R T R S E G G P S W K N G L M
 SEQ. ID. NO. 13 W T G L O L S V H V R R G Q Q A G N K T G

SEQ. ID. NO. 9 TGCACCAACTGTA 363
 SEQ. ID. NO. 10 ACGTGGTGCAT
 SEQ. ID. NO. 11 A P T V
 SEQ. ID. NO. 12 L H Q L Y
 SEQ. ID. NO. 13 C T N C

FIGURE 10

Lipman-Pearson Protein Alignment

Ktuple: 2; Gap Penalty: 4; Gap Length Penalty: 12

Seq1(1>107)	Seq2(1>111)	Similarity Index	Gap Number	Gap Length	Consensus Length
J591VK.PRO	MUVKV.PRO	60.4	2	2	109
(1>107)	(1>109)				

10 20 30 40 50
 NIVMTQSPKSMMSVGERVTLTCKAS-ENVVTVVSWYQQKPEQSPKLLIYGASNRYTGVP
 :I MTQSP.S:S S:G:RVT:TC:AS:::Y::WYQQK. SPKLLIY AS:.:GVP
 DIQMTQSPSSLASLGDRVTITCRASODDISNYLNWYQQKPGGSPKLLIYYASRLHSGYP
 10 20 30 40 50 60
 60 70 80 90 100
 DRFTGSGSATDFTLTSSVOAEDLADYHCGGYSY-PYTFGGGTKLEIK
 RE:GSGS:TD::LT:IS:::ED:A.Y C.QG::P TFGGGTKLEIK
 SRFSGSGSGTDYSLTISNLEQED:ATYFCQQGNTLPRTFGGGTKLEIK
 70 80 90 100

FIGURE 11



FIGURE 12